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OM protein - protein search, using sw model

Run on: March 17, 2003, 07:13:51 ; Search time 4.06107 Seconds
(without alignments)
194.050 Million cell updates/sec

Title: US-09-787-082-8

Perfect score: 119

Sequence: 1 GCCSNPVCHLEHSLNLTNG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	102	85.7	1 CXA2_CONMA	P56636 conus magus
2	61	51.3	66 1 CXA2_CONTE	Q9xzk7 conus texti
3	60.5	50.8	971 1 RECK_MOUSE	Q920j1 mus musculus
4	57.5	48.3	1 RECK_HUMAN	Q95980 homo sapien
5	55	46.2	69 1 CXA1_CONTE	Q9xzk6 conus texti
6	55	46.2	588 1 GRN_RAT	P23785 r granulus
7	54	45.4	16 1 CXA1_CONEP	P56638 conus epis
8	51	42.9	16 1 CXA1_CONAL	P56639 conus aulic
9	50	42.0	16 1 CXA3_CONAL	P56641 conus aulic
10	50	42.0	16 1 CXAB_CONPE	P50985 conus penna
11	48.5	40.8	1210 1 EGFR_MOUSE	Q01279 mus musculus
12	48	40.3	593 1 GRN_HUMAN	P28799 h granulus
13	47	39.5	18 1 CXA1_CONER	P50982 conus ermin
14	47	38.5	69 1 OXT1_OYIKI	P83288 oxyopes kit
15	47	39.5	566 1 EST1_PIG	Q29550 sus scrofa
16	45.5	38.2	1046 1 PSTA_DICDI	P11976 dictyostell
17	45	37.8	16 1 CXAA_CONPE	P50984 conus penna
18	45	37.8	72 1 CXA2_CONST	P28879 conus stria
19	44.5	37.4	434 1 SL54_BRAOL	P17841 brassica ol
20	44	37.0	19 1 CXR_CONTU	P58811 conus tulip
21	44	37.0	445 1 AD18_RAT	P97776 rattus norv
22	44	37.0	712 1 FBI1_CAEEL	Q77469 caenorhabdi
23	44	37.0	719 1 AD18_MOUSE	Q9r157 mus musculus
24	43	36.1	272 1 Y5T5_CAEEL	Q10037 caenorhabdi
25	43	36.1	452 1 AD11_XENLA	Q9ps23 xenopus lae
26	43	36.1	525 1 NAB2_YEAST	P2505 saccharomyc
27	43	36.1	586 1 LRE1_YEAST	P78325 saccharomyc
28	43	36.1	824 1 AD08_HUMAN	P78325 homo sapien
29	42.5	35.7	54 1 IOVO_ANHNO	P05565 aninga nov
30	42.5	35.7	54 1 IOVO_CIRAE	P05579 circus aeru
31	42.5	35.7	54 1 IOVO_DRONO	P05560 dromalus no
32	42.5	35.7	54 1 IOVO_GUIGU	P52246 guira copro
33	42.5	35.7	54 1 IOVO_GYPCO	P05578 gyps coprot

RESULT 1

ID	CXA2_CONMA	STANDARD;	PRT;	16 AA.
AC	P56636;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Alpha-conotoxin MII (M2).			
OS	Conus magus (Magus cone).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
OX	NCBI_TaxID=6492;			
RN	[1]			
RP	SEQUENCE, AND SYNTHESIS.			
RC	TISSUE=Venom;			
RX	MEDLINE=96205934; PubMed=8631783;			
RA	Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,			
RA	McIntosh J.M.;			
RT	"A new alpha-conotoxin which targets alpha3beta2 nicotinic			
RT	acetylcholine receptors."			
RL	J. Biol. Chem. 271:7522-7528(1996).			
RN	[2]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=98062282; PubMed=9398298;			
RA	Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;			
RT	"Three-dimensional solution structure of alpha-conotoxin MII, an			
RT	alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted			
RT	ligand."			
RL	Biochemistry 36:15693-15700(1997).			
RN	[3]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=99060038; PubMed=9843366;			
RA	Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,			
RA	Craik D.J.;			
RT	"Three-dimensional solution structure of alpha-conotoxin MII by NMR			
RT	spectroscopy: effects of solution environment on helicity."			
RL	Biochemistry 37:15621-15630(1998).			
CC	-!- FUNCTION: THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS			
CC	INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC			
CC	ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT			
CC	HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER			
CC	NACHR SUBUNIT COMBINATIONS.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Expressed by the venom duct.			
CC	-!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE			
CC	FAMILY.			
DR	PDB; IMII; 21-OCT-98.			
DR	PDB; IM2C; 13-JAN-99.			
KW	Postsynaptic neurotoxin; Neurotoxin; Toxin;			
KW	Acetylcholine receptor inhibitor; Amidation; 3D-structure.			
FT	DISULFID 2 8			
FT	DISULFID 3 16			
FT	MOD_RES 16 16			
FT	AMIDATION.			
SEQ	SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;			

P52268 haliaetus
P05577 haliaetus i
P52263 pavo muticu
P05564 phalacrocor
P52257 pygocallis
P05558 rhea americ
P05563 rheniscus
P05609 pavo crista
Q9x9e0 erwinia chr
P74330 synechocyst
P13508 caenorhabdi
P50983 conus imper

Query Match 85.7%; Score 102; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCSNPVCHELSNLC 16
DB 1 GCCSNPVCHELSNLC 16

RESULT 2
CX22_CONTE STANDARD; PRT; 66 AA.
AC Q9X2K7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-type conotoxin Tx2 precursor.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-Venom duct;
RX MEDLINE=20037955; PubMed=10573284;
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
RT "Conopeptides from Conus striatus and Conus textile by cDNA
cloning";
RL Peptides 20:1139-1144(1999).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
FAMILY.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).

EMBL; AF146353; AD31913.1; --
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 48 POTENTIAL.
FT PEPTIDE 49 66 ALPHA-TYPE CONOTOXIN TX2.
FT DISULFID 51 57 BY SIMILARITY.
FT DISULFID 52 65 BY SIMILARITY.
SQ SEQUENCE 66 AA; 7254 MW; EDDBS9BBAB94F26F CRC64;

Query Match 51.3%; Score 61; DB 1; Length 66;
Best Local Similarity 46.7%; Pred. No. 0.059;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCSPNVCHELSNLC 16
DB 51 CCSPNVCHELSNLC 65

RESULT 3
RECK_MOUSE STANDARD; PRT; 971 AA.
AC Q9Z0J1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor
(nRECK).

GN RECK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
invasion by the membrane-anchored glycoprotein RECK";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
by suppressing MMP-9 secretion, and by direct inhibition of its
enzymatic activity. RECK down-regulation by oncogenic signals may
facilitate tumor invasion and metastasis. Appears to also
regulate MMP-2 and MT1-MMP, which are involved in cancer
progression (By similarity).
CC -!- SUBUNIT: Interacts with MMP-9.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- DEVELOPMENTAL STAGE: In E10.5 embryos the RECK protein is widely
expressed in mesenchymal tissues and is relatively abundant in the
marginal zone of the neural tube and large blood vessels such as
the aorta.
CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.

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EMBL; AB006960; BAA34061.1; --
MGD; MGI:1855698; Reck.
DR InterPro; IPR002350; Kazal.
DR Pfam; PF00050; Kazal; 2.
DR SMART; SM00280; KAZAL; 2.
DR PROSITE; PS00282; KAZAL; 1.
KW Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
KW Membrane; Anti-oncogene; Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 942 REVERSION-INDUCING CYSTEINE-RICH PROTEIN
WITH KAZAL MOTIFS.
FT PROPEP 943 971 REMOVED IN MATURE FORM (POTENTIAL).
FT LIPID 942 942 GPI-ANCHOR (POTENTIAL).
FT DOMAIN 633 677 KAZAL-LIKE 1.
FT DOMAIN 704 750 KAZAL-LIKE 2 (DEGENERATE).
FT DOMAIN 751 787 KAZAL-LIKE 3 (DEGENERATE).
FT DOMAIN 37 338 5 X KNOT REPEATS.
FT REPEAT 37 84 KNOT 1.
FT REPEAT 104 141 KNOT 2.
FT REPEAT 151 197 KNOT 3.
FT REPEAT 216 263 KNOT 4.
FT REPEAT 292 338 KNOT 5.
FT DISULFID 635 654 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT DISULFID 643 677 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 971 AA; 106134 MW; 2FC8EBE38A20F86D CRC64;

Query Match 50.8%; Score 60.5; DB 1; Length 971;
Best Local Similarity 68.8%; Pred. No. 0.65;
Matches 11; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 5 NPVC---HLEHSNLC 17

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Db 721 DPVCDTHMHSNLC7 736
:|||||
RESULT 4
RECK_HUMAN STANDARD; PRT; 971 AA.
AC O95980; Q8W37;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reversion-inducing cysteine-rich protein with kazal motifs precursor
DE (hRECK) (Suppressor of tumorigenicity 15) (ST15).
GN RECK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND N-GLYCOSYLATION.
RC TISSUE=Fibroblast;
RX MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
RT invasion by the membrane-anchored glycoprotein RECK.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
RN [2]
RP SEQUENCE OF 363-971 FROM N.A.
RA Kimberley A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
CC by suppressing MMP-9 secretion and by direct inhibition of its
CC enzymatic activity. RECK down-regulation by oncogenic signals may
CC facilitate tumor invasion and metastasis. Appears to also
CC regulate MMP-2 and MT1-MMP, which are involved in cancer
CC progression.
CC -!- SUBUNIT: Interacts with MMP-9.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Expressed in various tissues and untransformed
CC cells. It is undetectable in tumor-derived cell lines and
CC oncogenically transformed cells.
CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; D50406; BRA34060.1; -.
DR EMBL; AL158830; CAD13384.1; -.
DR GenBank; HGNC:11345; RECK.
DR MIM; 605227; -.
DR HSSP; P80424; 1AN1.
DR InterPro; IPR002350; kazal.
DR SMART; SM00280; KAZAL; 3.
DR SMART; SM00011; VWC_def; 1.
DR PROSITE; PS00282; KAZAL; 1.
KW Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
KW Membrane; Anti-oncogene; Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 942 REVERSION-INDUCING CYSTEINE-RICH PROTEIN
FT FT WITH KAZAL MOTIFS.
FT PROPEP 943 971 REMOVED IN MATURE FORM (POTENTIAL).
FT LIPID 942 942 GPI-ANCHOR (POTENTIAL).
FT DOMAIN 632 677 KAZAL-LIKE 1.
FT DOMAIN 708 750 KAZAL-LIKE 2 (DEGENERATE).
FT DOMAIN 753 787 KAZAL-LIKE 3 (DEGENERATE).
FT DOMAIN 37 338 5 X KNOT REPEATS.

Query Match 48.3%; Score 57.5; DB 1; Length 971;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 10; Conservative 3; Mismatches 0; Indels 3; Gaps 1;

QY 5 NPVC---HLEHSNLC7 17
:||||| :||:|||||
Db 721 DPVCDTHMHSNLC7 736

RESULT 5
CXAL_CONTE STANDARD; PRT; 69 AA.
AC O9XZK6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-type conotoxin Tx1 precursor.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RX MEDLINE=20037955; PubMed=10573284;
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
RT "Conopeptides from Conus striatus and Conus textile by cDNA
RT cloning.";
RL Peptides 20:1139-1144(1999).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF146352; AAD31912.1; -.
DR Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Signal; Amidation.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 48 POTENTIAL.
FT PEPTIDE 49 66 ALPHA-TYPE CONOTOXIN TX1.
FT DISULFID 51 57 BY SIMILARITY.
FT DISULFID 52 65 BY SIMILARITY.
FT MOD_RES 66 66 AMIDATION (G-67 PROVIDE AMIDE GROUP).
SQ SEQUENCE 69 AA; 7442 MW; E36ECE90BF1B56B0 CRC64;

Query Match 46.2%; Score 55; DB 1; Length 69;
Best Local Similarity 53.3%; Pred. No. 0.38;

FT REPEAT 37 84 KNOT 1.
FT REPEAT 104 141 KNOT 2.
FT REPEAT 151 197 KNOT 3.
FT REPEAT 216 263 KNOT 4.
FT REPEAT 292 338 KNOT 5.
FT DISULFID 635 654 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT DISULFID 643 677 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 971 AA; 106456 MW; 173D47D6AE6F834 CRC64;
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Best Local Similarity 43.8%; Pred. No. 0.15;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCCSNPVCHEHSLNC 16
    ||||| |::: |
Db 1 GCCSDPRCANNPDYC 16

RESULT 8
CXAL_CONAL
ID CXAL_CONAL STANDARD; PRT; 16 AA.
AC P56639.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin AuIB.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;

RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).
CC -|- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom duct..
CC -|- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
CC -|- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR HSSP; P50984; lPEN.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 8
FT MOD_RES 3 16
FT MOD_RES 16 16
SQ SEQUENCE 16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;

Query Match 42.9%; Score 51; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.38;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCSNPVCHEHSLNC 16
    ||||| |::: |
Db 1 GCCSYPCFATNSDYC 16

RESULT 9
CXAL_CONAL
ID CXAL_CONAL STANDARD; PRT; 16 AA.
AC P56641.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin AuIC.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;

RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin AuIC selectively blocks alpha3 beta4 nicotinic
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).
CC -|- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom duct..
CC -|- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
CC -|- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR HSSP; P50984; lPEN.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 8
FT MOD_RES 3 16
FT MOD_RES 16 16
SQ SEQUENCE 16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;

Query Match 42.9%; Score 51; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.38;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCSNPVCHEHSLNC 16
    ||||| |::: |
Db 1 GCCSYPCFATNSDYC 16

RESULT 9
CXAL_CONAL
ID CXAL_CONAL STANDARD; PRT; 16 AA.
AC P56641.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin AuIB.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;

RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).
CC -|- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom duct..
CC -|- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.
CC -|- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR HSSP; P50984; lPEN.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 8
FT MOD_RES 3 16
FT MOD_RES 16 16
SQ SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;

Query Match 42.0%; Score 50; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.52;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCCSNPVCHEHSLNC 16
    ||||| |::: |
Db 1 GCCSYPCFATNSDYC 16

RESULT 10
CXAL_CONPE
ID CXAL_CONPE STANDARD; PRT; 16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin PnIB.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;

RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULEFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.H., Gehrman J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
RT comparison with alpha-conotoxins PnIA and GI.";
RL Biochemistry 36:11323-11330(1997).
CC -|- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PDB: 1AKG; 20-MAY-98.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;

Query Match 42.0%; Score 50; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.52;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCSNPVCHLEHSLNC 16
   ||||| | | | | |
Db 1 GCCSLPPCALSNPDYC 16

RESULT 11
EGFR_MOUSE
ID EGFR_MOUSE STANDARD; PRT; 1210 AA.
AC Q01279;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Epidermal growth factor receptor precursor (EC 2.7.1.112).
GN EGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=93026370; PubMed=1408137;
RA Avivi A., Skorecki K., Yayon A., Givol D.;
RT "Promoter region of the murine fibroblast growth factor receptor 2
RT (bek/KGFR) gene.";
RL Oncogene 7:1957-1962(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c, and CD-1; TISSUE=Liver, and Decidua;
RX MEDLINE=93126380; PubMed=7678348;
RA Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
RT "Expression of the epidermal growth factor receptor gene is regulated
RT in mouse blastocysts during delayed implantation.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Hibbs M.L.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/C3; TISSUE=Liver;
RX MEDLINE=94170986; PubMed=8125255;
RA Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
RA Jenkins N.A., Lee D.C.;
RT "The mouse waved-2 phenotype results from a point mutation in the EGF
RT receptor tyrosine kinase.";
RL Genes Dev. 8:399-413(1994).
RN [5]
RP SEQUENCE OF 1-714 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91232866; PubMed=2030916;
RA Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;
RT "Comparison of EGF receptor sequences as a guide to study the ligand
RT binding site.";
RL Oncogene 6:673-676(1991).

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RN [6]
RP SEQUENCE OF 969-1117 FROM N.A.
RC STRAIN=C3H;
RA Eisinger D.P., Serrero G.;
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
CC AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
CC VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- MISCELLANEOUS: Binding of EGF to the receptor leads to
CC dimerization, internalization of the EGF-receptor complex,
CC induction of the tyrosine kinase activity, stimulation of cell DNA
CC synthesis, and cell proliferation.
CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC -----
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CC -----
DR EMBL; X78987; CAA55587.1; -.
DR EMBL; U03425; AAA17899.1; -.
DR EMBL; X59698; CAA42219.1; -.
DR EMBL; L06864; AAA53029.1; -.
DR EMBL; Z12608; CAA78249.1; -.
DR HSPF; F11362; IFGK.
DR MGD; MGI:95294; Egfr.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
KW Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 1210 EPIDERMAL GROWTH FACTOR RECEPTOR.
FT DOMAIN 25 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 670 POTENTIAL.
FT DOMAIN 671 1210 CYTOPLASMIC (POTENTIAL).
FT REPEAT 75 300 APPROXIMATE.
FT REPEAT 390 600 APPROXIMATE.
FT DOMAIN 1028 1071 SER-RICH.
FT DOMAIN 714 981 PROTEIN KINASE.
FT NP_BIND 720 728 ATP (BY SIMILARITY).
FT BINDING 747 747 ATP (BY SIMILARITY).
FT ACT_SITE 839 839 BY SIMILARITY.
FT DISULFID 190 199 BY SIMILARITY.
FT DISULFID 194 207 BY SIMILARITY.
FT DISULFID 215 223 BY SIMILARITY.
FT DISULFID 219 231 BY SIMILARITY.
FT DISULFID 232 240 BY SIMILARITY.
FT DISULFID 236 248 BY SIMILARITY.
FT DISULFID 251 260 BY SIMILARITY.
FT DISULFID 264 291 BY SIMILARITY.
FT DISULFID 295 307 BY SIMILARITY.
FT DISULFID 311 326 BY SIMILARITY.
FT DISULFID 329 333 BY SIMILARITY.
FT DISULFID 506 515 BY SIMILARITY.
FT DISULFID 510 523 BY SIMILARITY.
FT DISULFID 526 535 BY SIMILARITY.

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FT DISULFID 539 555 BY SIMILARITY.
FT DISULFID 558 571 BY SIMILARITY.
FT DISULFID 562 579 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT DISULFID 595 617 BY SIMILARITY.
FT DISULFID 620 628 BY SIMILARITY.
FT DISULFID 624 636 BY SIMILARITY.
FT MOD_RES 680 680 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT MOD_RES 1092 1092 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1110 1110 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1172 1172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1197 1197 PHOSPHORYLATION (AUTO-, MAJOR SITE) (BY SIMILARITY).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 528 528 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 19 19 C -> S (IN REF. 2).
FT CONFLICT 539 539 C -> W (IN REF. 5).
FT CONFLICT 991 991 L -> F (IN REF. 4).
FT CONFLICT 1116 1117 HP -> DR (IN REF. 6).
SQ SEQUENCE 1210 AA; 134853 MR; 690E20D46DF2D2F5 CRC64;

Query Match 40.8%; Score 48.5; DB 1; Length 1210;
Best Local Similarity 62.5%; Pred. NO. 31;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 4 SNPVCHELSNCTNG 19
DB 613 ANNCHLCHAN-CTYG 627

RESULT 12
GRN_HUMAN
ID GRN_HUMAN STANDARD; PRT; 593 AA.
AC P28799; P23781; P23782; P23783; P23784; Q9BWE7;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granulins precursor (Acrogranin) [Contains: Paragranulin; Granulin 1 (Granulin G); Granulin 2 (Granulin F); Granulin 3 (Granulin B); Granulin 4 (Granulin A); Granulin 5 (Granulin C); Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
DE GRN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=92179253; PubMed=1542665;
RA Bhandari V., Palfrey R.G.E., Bateman A.;
RT "Isolation and sequence of the granulin precursor cDNA from human bone marrow reveals tandem cysteine-rich granulin domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).
RN [2]
RP REVISIONS, SEQUENCE FROM N.A.
RX MEDLINE=93038704; PubMed=1417868;
RA Bhandari V., Bateman A.;
RT "Structure and chromosomal location of the human granulin gene.";
RL Biochem. Biophys. Res. Commun. 188:57-63(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92317004; PubMed=1618805;
RA PLOWMAN G.D., GREEN I.M., NEUBAUER M.G., BUCKLEY S.D., McDONALD V.L.,

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RA Todaro G.J., Shoyab M.;
RT "The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.";
RL J. Biol. Chem. 267:13073-13078(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yu W., Gibbs R.A.;
RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Cervix, and Lung;
RA Strausberg R.;
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.
RC TISSUE=Leukocyte;
RX MEDLINE=91097544; PubMed=2268320;
RA Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S.;
RT "Granulins, a novel class of peptide from leukocytes.";
RL Biochem. Biophys. Res. Commun. 173:1161-1168(1990).
CC -!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
CC -!- FUNCTION: GRANULIN A PROMOTES PROLIFERATION OF THE EPITHELIAL CELL LINE A431 IN CULTURE WHILE GRANULIN B ACTS AS AN ANTAGONIST TO GRANULIN A, INHIBITING THE GROWTH.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: IN MYELOGENOUS LEUKEMIC CELL LINES OF PROMONOCYTIC, PROMYELOCYTIC, AND PROERYTHROID LINEAGE, IN FIBROBLASTS, AND VERY STRONGLY IN EPITHELIAL CELL LINES. PRESENT IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY.
CC -!- PTM: GRANULINS ARE DISULFIDE BRIDGED.
CC
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CC
DR EMBL; M75161; AAA58617.1; ALT_SEQ.
DR EMBL; X62320; CAA44196.1; -.
DR EMBL; AF055008; AAC09359.1; -.
DR EMBL; BC000324; AAH00324.1; -.
DR EMBL; BC010577; AAH10577.1; -.
DR PIR; A38118; GYHU.
DR PIR; D36698; D36698.
DR PIR; JC1284; JC1284.
DR Genew; HGNC:4601; GRN.
DR MIM; 138945; -.
DR InterPro; IPR000118; Granulin.
DR Pfam; PF00396; granulin; 7.
DR SMART; SM00277; GRAN; 7.
DR PROSITE; PS00799; GRANULINS; 7.
KW Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
KW Polymorphism.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 593 ACROGRANIN.
FT PEPTIDE 18 747 PARAGRANULIN.
FT PEPTIDE 258 7113 GRANULIN 1.
FT PEPTIDE 7123 7179 GRANULIN 2.
FT PEPTIDE 206 261 GRANULIN 3.
FT PEPTIDE 281 336 GRANULIN 4.
FT PEPTIDE 364 7417 GRANULIN 5.
FT PEPTIDE 7518 7573 GRANULIN 6.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT VARSPLIC 377 531 MISSING (IN ISOFORM 2).
FT VARIANT 454 454 G -> Q.
FT CONFLICT 219 219 /FTid=VAR_003445.
FT CONFLICT 386 386 S -> H (IN REF. 6).
FT CONFLICT 386 386 W -> H (IN REF. 6).
SQ SEQUENCE 593 AA; 63473 MW; 4B402BDB16DE2819 CRC64;

Query Match 40.3%; Score 48; DB 1; Length 593;
Best Local Similarity 42.9%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

Qy 1 GCCSNP--VCHLEHNLCTNG 19
   ||| | || : | : |
Db 387 GCCPIPEAVCCSDHQCPCQ 407

RESULT 13
CXAL_CONER
ID CXAL_CONER STANDARD; PRT; 18 AA.
AC P50982;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin EI.
OS Conus ermineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96062516; PubMed=7578057;
RA Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Groebe D.R.,
RA Abramson S.N., McIntosh J.M.;
RT "Alpha-conotoxin EI, a new nicotinic acetylcholine receptor
RT antagonist with novel selectivity.";
RL Biochemistry 34:14519-14526(1995).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -!- SUBUNIT: Binds nicotinic acetylcholine receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Hydroxylation.
FT DISULFID 4 10
FT DISULFID 5 18
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 2082 MW; 60A61A6C427A6B5E CRC64;

Query Match 39.5%; Score 47; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.4;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCNSNPVCHLEHNL 16
   || | | : : |
Db 4 CCYHPTCNMNPQIC 18

RESULT 14
OXTL_OXYKI
ID OXTL_OXYKI STANDARD; PRT; 69 AA.
AC P83288;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Oxytoxin 1 (Oxyt1).
OS Oxyopes kitabensis (Wolf spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosidae; Oxyopidae; Oxyopes.
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OX NCBI_TaxID=184771;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
RP SPECTROMETRY, AND CIRCULAR DICHROISM ANALYSIS.
RC TISSUE=Venom;
RX PubMed=11976325;
RA Corzo G., Villegas E., Gomez-Lagunas F., Possani L.D.,
RA Belokoneva O.S., Nakajima T.;
RT "Oxyopinins, large amphipathic peptides isolated from the venom of the
RT wolf spider Oxyopes kitabensis with cytolytic properties and positive
RT insecticidal cooperativity with spider neurotoxins.";
RL J. Biol. Chem. 277:23627-23637(2002).
CC -!- FUNCTION: Is both paralytic and lethal, when injected into
CC lepidopteran larvae. Probably blocks voltage-gated sodium
CC channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- PTM: Five disulfide bonds are present.
CC -!- MASS SPECTROMETRY: MW=8059.25; METHOD=MALDI.
CC -!- MISCELLANEOUS: LD(50) is 41.1 mg/kg by subcutaneous
CC injection.
KW Sodium channel inhibitor; Toxin; Neurotoxin.
SQ SEQUENCE 69 AA; 8069 MW; 2C3FCF05BA330159 CRC64;

Query Match 39.5%; Score 47; DB 1; Length 69;
Best Local Similarity 50.0%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCNSNPVCHLEHNL 15
   || | | : |
Db 17 CCKNHHCPCYSNV 30

RESULT 15
ESTL_PIG
ID ESTL_PIG STANDARD; PRT; 566 AA.
AC Q29550;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Liver carboxylesterase precursor (EC 3.1.1.1) (Proline-beta-
DE naphthylamidase).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92070571; PubMed=1959668;
RA Matsushima M., Inoue H., Ichinose M., Tsukada S., Miki K.,
RA Kurokawa K., Takahashi T., Takahashi K.;
RT "The nucleotide and deduced amino acid sequences of porcine liver
RT proline-beta-naphthylamidase. Evidence for the identity with
RT carboxylesterase.";
RL FEBS Lett. 293:37-41(1991).
CC -!- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
CC ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O -> an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC -----
DR EMBL; X63323; CAA44929.1; -.
DR HSSP; P21836; IMAH.
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DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR00379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW signal; Multigene family.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 566 LIVER CARBOXYLESTERASE.
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 467 467 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 88 117 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 563 566 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 566 AA; 62016 MW; BE046545307DEDE5 CRC64;

Query Match 39.5%; Score 47; DB 1; Length 566;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 CCSNPVCHLEHSLCTNG 19
 || :|| | :|||
Db 88 CCQDPVVEQMTSLFTNG 105

Search completed: March 17, 2003, 07:24:19
Job time : 5.06107 secs

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